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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 22:43:56 ; Search time 1498 Seconds
(without alignments)
11276.297 Million cell updates/sec

Title: US-09-807-933B-13

Perfect score: 1043

Sequence: 1 ggatcctgggacaagatgaa.....cgaaagtaaacgcagatccc 1043

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estc:*
9: gb_esti:*
10: gb_est2:*
11: gb_hc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_othr:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	174.6	16.7	691	10	BE585661
2	133.4	12.8	450	13	BI200729
3	122.2	11.7	444	13	BI190695
4	114.2	10.9	426	13	BI187295
5	83.2	8.0	215	13	BI190568
6	63.4	6.1	606	10	AW057101

7	62.8	6.0	274	13	BI188678
8	62.8	6.0	280	13	BI190362
9	62.8	6.0	289	13	BI189728
10	62.8	6.0	289	13	BI191461
11	62.8	6.0	299	13	BI187393
12	60.4	5.8	500	10	AW565843
13	59.8	5.7	406	10	BE355499
14	59.2	5.7	1490	11	AV103602
15	58.4	5.6	490	14	BQ743825
16	58.4	5.6	605	17	A2640388
17	58.2	5.6	559	13	BM324075
18	58.2	5.6	585	10	BE470936
19	58.2	5.6	607	13	BM323555
20	58.2	5.5	627	12	BG608096
21	57.4	5.5	306	12	BE898613
22	57.2	5.5	582	10	BE583904
23	56.8	5.4	539	13	BM326380
24	56.2	5.4	547	10	AW672247
25	56.2	5.4	610	13	BM324963
26	56.2	5.4	640	10	AV946870
27	56	5.4	487	10	BE367299
28	55.8	5.3	243	10	AW285303
29	55.6	5.3	582	10	AV941765
30	55.6	5.3	584	10	AW671327
31	55.6	5.3	925	17	CNS0091P
32	55.4	5.3	383	12	BF484001
33	55.4	5.3	588	9	AL823173
34	55.4	5.3	648	10	BE517305
35	55.4	5.3	648	13	BM368064
36	55	5.3	401	13	BM348963
37	55	5.3	458	13	BM335613
38	55	5.3	508	13	BM349604
39	55	5.3	539	13	BM336729
40	54.8	5.3	749	14	BQ744212
41	54.6	5.2	577	13	BM075237
42	54.6	5.2	654	14	BQ294885
43	54.6	5.2	668	14	BQ788781
44	54.4	5.2	537	9	AL821349
45	54.4	5.2	619	13	BM442102

ALIGNMENTS

RESULT 1
BE585661
LOCUS
DEFINITION
EST#6PSP6_D02_d2_014 KSU wheat Fusarium graminearum infected spike
CDNA library Triticum aestivum cDNA clone EST#6PSP6_D02_d2_014,
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BE585661
BE585661.1 GI:9838604
EST.
bread wheat.
Triticum aestivum
Fusarium graminearum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
REFERENCE
AUTHORS
TITLE
The structure and function of the expressed portion of the wheat
genomes - Kansas State University. Fusarium graminearum infected
spike CDNA library
JOURNAL
COMMENT
Unpublished (2000)
Contact: John Fellers
US Department of Agriculture, Agriculture Research Service, Plant
Science and Entomology Unit
Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State
University, Manhattan, KS 66506, USA
Tel: 785-532-2367
Fax: 785-532-6167
Email: jpf@alfalfa.ksu.edu
Sequence have been trimmed to remove vector sequence and low

	linear	EST 10-JUL-2001
Bt190695	444 bp mRNA	
Locus	Fusarium sporotrichioides Tri 10 overexpressed cDNA	
Definition	i3g10fs.v1	

RESULT 2					
B1200729					
LOCUS	B1200729	450 bp	mRNA	linear	EST 10-JUL-2001
DEFINITION	Fusarium sporotrichoides Tri 1 overexpressed cDNA o1f05fs.r1				
	est=biocides cDNA clone olf05fs 5', mRNA				

library Fusarium sporotrichioides cDNA clone i3g10fs 5', mRNA
sequence.
ACCESSION B1190695
VERSION B1190695.1 GI:14664374
KEYWORDS
SOURCE
ORGANISM
Fusarium sporotrichioides.
Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.
REFERENCE
1 (bases 1 to 444)
AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
,M. and Roe,B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
576 3e-59 gi|1170140|sp|p45699 PUTATIVE ENDOGLUCANASE TYPE
KPRECUSOR (EN
Seq primer: T3.
Location/Qualifiers
FEATURES
source
1..444
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="i3g10fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBlueScript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBlueScript
XhoI; 3' end of cDNA cloned into XhoI site of pBlueScript"
BASE COUNT 85 a 127 c 92 g 140 t
ORIGIN
Query Match 11.7%; Score 122.2; DB 13; Length 444;
Best Local Similarity 63.4%; Pred. No. 3.3e-15;
Matches 187; Conservative 0; Mismatches 108; Indels 0; Gaps 0;
QY 395 GTGGCGCTAGCGCAAGCGCTCACTACCGCTACTGGGACTGCTGCAAGGCTTCGTGCT 454
DB 150 GTGCTGCTTCTGAACTGGCCACTCTACTCGATCTGGGACTGCTGCAAGCCTTCTTGCT 209
QY 455 CGTGGCCCGGCAAGGCTAAGCTCAGCTCGCCTGTCAAGTCTCTGCAACAAGGACGGGTCA 514
DB 210 CTTGGAGCGCAAGGCTAAGTCAAGTCAGCGCCCTGCTGACTTGTGACACAAGATAACC 269
QY 515 CGCTCTTAGCGACTCAAGCCAGTCCGGCTGCAACGGCGGCAACTCTCATATGTGCA 574
DB 270 CTATCACTAACCTGAAACGCTGTCAACGGTTGTGAGGGTGTGCTGCTTATGCTTGA 329
QY 575 ACACAACAGCAGCATGGCTGTCAACGACAACTTGTACGTTTCGCTGCGGTGCCA 634
DB 330 CCAACTACTCCCGTGGGCTGTCAACGACACTTGTCTACGTTTCGCTGCTACCAAGC 389
QY 635 TTAGCGCGGTGGCGAGACCGGTGCTGCTGCTCTCTGCTTCGAGCTCACCTTCAAC 689
DB 390 TTGCTGGTGTAGTGAGGCCAGCTGTGCTGTGCTGTGCTGTCTCTCACCTTCAAC 444

RESULT 4
B1187295
LOCUS
DEFINITION
426 bp mRNA linear EST 10-JUL-2001
alhlifs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone alhlifs 5', mRNA
sequence.
ACCESSION
B1187295
VERSION
B1187295.1 GI:14660974

EST.
Fusarium sporotrichioides.
Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.
REFERENCE
1 (bases 1 to 426)
AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
,M. and Roe,B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Other_ESTs: alhlifs.f1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
565 5e-58 gi|1170140|sp|p45699 PUTATIVE ENDOGLUCANASE TYPE
KPRECUSOR (EN
Seq primer: T3
High quality sequence stop: 338.
Location/Qualifiers
FEATURES
source
1..426
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="alhlifs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBlueScript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBlueScript
XhoI; 3' end of cDNA cloned into XhoI site of pBlueScript"
BASE COUNT 82 a 119 c 91 g 134 t
ORIGIN
Query Match 10.9%; Score 114.2; DB 13; Length 426;
Best Local Similarity 62.4%; Pred. No. 1.4e-13;
Matches 179; Conservative 0; Mismatches 108; Indels 0; Gaps 0;
QY 395 GTGGCGCTAGCGCAAGCGCGTCACTACCGCTACTGGGACTGCTGCAAGGCTTCGTGCT 454
DB 140 GTGCTGCTTCTGAAAGTGCCACTCTACTCGATCTGGGACTGCTGCAAGCCTTCTTGCT 199
QY 455 CGTGGCCCGGCAAGGCTAAGCTAAGTCAAGTCTCTGCAACAAGGACGGGTCA 514
DB 200 CTTGGAGCGCAAGGCTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 259
QY 515 CGCTCTTAGCGACTTCAAGCCAGTCCGGCTGCAACGGCGGCAACTCTCATATGTGCA 574
DB 260 CTATCACTAACCTGAAACGCTGTCAACGGTTGTGAGGGTGTGCTGCTTATGCTTGA 319
QY 575 ACACAACAGCAGCATGGCTGTCAACGACAACTTGTCTTACGTTTCGCTGCGGTGCCA 634
DB 320 CCAACTACTCCCGTGGGCTGTCAACGACACTTGTCTTACGTTTCGCTGCTACCAAGC 379
QY 635 TTAGCGCGGTGGCGAGACCGGTGCTGCTGCTCTCTGCTTCGAGCTC 681
DB 380 TTGCTGGTGTAGTGAGGCCAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 426

RESULT 5
B1190568
LOCUS
DEFINITION
215 bp mRNA linear EST 10-JUL-2001
i2ellifs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone i2ellifs 5', mRNA
sequence.
ACCESSION
B1190568
VERSION
B1190568.1 GI:14664247
KEYWORDS
SOURCE
Fusarium sporotrichioides.

ORGANISM	Fusarium sporotrichioides
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium.
AUTHORS	1 (bases 1 to 215)
TITLE	Ren.Q., Tag.A., Peplow.A., Lai.H., Kupfer.C., Peterson.A., Beremand
JOURNAL	,M. and Roe.B.
COMMENT	Analysis of a Fusarium sporotrichioides EST database Other ESTs: i2el1fs.f1 Unpublished (2001) Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu Department of Chemistry and Biochemistry Advanced Center for Genome Technology, University of Oklahoma 620 Parrington Oval, Norman, OK 73019, USA Tel: 405 325 4912 Fax: 405 325 7762 Email: broe@ou.edu Contact: Dr. Marian Beremand regarding clone availability Included is the best homolog from a blastx search of Genbank nr 04-09-01 363 7e-35 g1 1170140 sp P45699 PUTATIVE ENDOGLUCANASE TYPE KPRECURSOR (EN Seq primer: T3 High quality sequence stop: 156. Location/Qualifiers 1..215 /organism="Fusarium sporotrichioides" /strain="Tri 10" /db xref="taxon:5514" /clone="i2el1fs" /clone lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library" /note="vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript ; 3' end of cDNA cloned into XhoI site of pBluescript" 44 a 61 c 53 g 56 t 1 others
BASE COUNT	44 a 61 c 53 g 56 t 1 others
ORIGIN	
Query Match	8.0%; Score 83.2; DB 13; Length 215;
Best Local Similarity	63.5%; Pred. No. 2.6e-07;
Matches 127; Conservative	0; Mismatches 73; Indels 0; Gaps 0;
QY	427 TACTGGGACTCTGCAAGGCTTGTGCTGTCGGCCGGCAAGCTACGTCAGCTCGCCT 486
Db	1 TACTGGGACTCTGCAAGGCTTGTGCTGTCGGCCGGCAAGCTAAAGTCAGCGCCCT 60
QY	487 GTCAGTCTGCAACAGGCGCTACCGCTCTTAGCGACTCCAAACGCCAGTCGCGC 546
Db	61 GCTCTGACTTGTGCAACAGATACCTATCTACTACCTGACGCTGTCACGGTTGT 120
QY	547 TGCACAGCGCGCAACTCCTATGTCACGACCAACAGCATGGGCTGTCAACGACAC 606
Db	121 GAGGCTGTGTTCTGCTTATGCTTGCACCACTACTCCCGTGGGCTGTCAACGAC 180
QY	607 CTTGCTTACGTTTCGTCGC 626
Db	181 CTTGCTTACGTTTCGTCGC 200
RESULT 6	
AW057101	606 bp mRNA linear EST 29-SEP-1999
LOCUS	6000801.y1 660 - Mixed stages of anther and pollen Zea mays cDNA,
DEFINITION	mRNA sequence.
ACCESSION	AW057101
VERSION	AW057101.1 GI:5932740
KEYWORDS	EST.
SOURCE	Zea mays.
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 606)
REFERENCE	Walbot.V
AUTHORS	Maize ESTs from various cDNA libraries sequenced at Stanford
TITLE	
University	Unpublished (1999)
Contact: Walbot V	
Department of Biological Sciences	
Stanford University	
855 California Ave, Palo Alto, CA 94304, USA	
Tel: 650 723 2227	
Fax: 650 725 8221	
Email: walbot@stanford.edu	
Plate: 660008 row: G column: 01.	
Location/Qualifiers	
1..606	
/organism="Zea mays"	
/cultivar="Ohio43"	
/db xref="taxon:4577"	
/clone lib="660 - Mixed stages of anther and pollen"	
/tissue_type="whole premiotic anthers to pollen shed"	
/dev_stage="premiotic anthers to pollen shed"	
/lab_host="XLOLR"	
/note="Organ: anthers; Vector: Lambda Zap; Site 1: EcoRI; Site 2: XhoI; Anther and pollen cDNA library. Directionally sequenced with 5' end at the EcoRI site. Created by Amie Franklin."	
BASE COUNT	119 a 229 c 176 g 81 t 1 others
ORIGIN	
Query Match	6.1%; Score 63.4; DB 10; Length 606;
Best Local Similarity	46.4%; Pred. No. 0.0044;
Matches 205; Conservative	0; Mismatches 237; Indels 0; Gaps 0;
QY	498 CAACAGACCGGTCACCGCTCTTAGCGACTCCAAACGCCAGTCCGGCTCAACGGCGG 557
Db	134 CAAGTACAGTCCAGCTCGGCATCTTCGACCGCGAGTCAAGCCGCTCGCGGACAGC 193
QY	558 CAATCTCTACATGTCAACGACCAACAGCCATGGGCTGTCAACGACAACTTGTCTTACGG 617
Db	194 CATCTCCGTCGACGCGCAAGGTCTCAAGGTCTGTCCGACCGCAACCCAGCACTGCC 253
QY	618 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 677
Db	254 GTGGGGCGAGTCTCGGCATCGACCTCTCATCGAGGGCACCGGCGTCTTCGTGACCGGA 313
QY	678 GCTCACTTCACTCCACCGGTTGTGCGCAAGAGATGGTGTGCTCAGGTCAACCAAC 737
Db	314 GGGGGGGGAGACATCCAGCGGGGCGCAAGAGGTGTCTCATCGCGCCCGCGCAA 373
QY	738 TGGCGGTGACTTGGGAGCTGACCGGTGCGCCACTTCATCTCCAGATGCCCGCGCGCG 797
Db	374 GGGCGACATCCCACTAGCTGCTGCGGTCTAAATCCGACCACTAGTAAACCCGAGGCC 433
QY	798 GCTGCGCATTTCAACGGATGCTGCTCCAGTGGGGCGCTCCCAACGAGCGGTGGGGTTC 857
Db	434 CATCATCAGCAAGCGCTCTCTGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 493
QY	858 GCGCTACGGCGGCATCAGCTCCGCGAGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 917
Db	494 CCAAAAGTTTGGCATCATCAAGGGCACCATGACCAACCACTCTCTACACCGGACCA 553
QY	918 CGGCTCAAGTGGCGCTTCAAC 939
Db	554 GAGTCTGTCGACCGGAGCCACC 575
RESULT 7	
Bi188678	274 bp mRNA linear EST 10-JUL-2001
LOCUS	d2c10fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
DEFINITION	library Fusarium sporotrichioides cDNA clone d2c10fs 5', mRNA
ACCESSION	sequence.
VERSION	Bi188678
KEYWORDS	EST.
SOURCE	Fusarium sporotrichioides.

ORGANISM Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.
REFERENCE 1 (bases 1 to 274)
AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
,M. and Roe,B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
303 1e-27 gi|1170140|sp|p45699 PUTATIVE ENDOGLUCANASE TYPE
KPRECURSOR (EN
Seq primer: T3
High quality sequence stop: 102.
FEATURES
source Location/Qualifiers
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/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="d2c10fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
XhoI; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 62 a 80 c 49 g 83 t
ORIGIN
Query Match 6.0%; Score 62.8; DB 13; Length 274;
Best Local Similarity 71.9%; Pred. No. 0.0044;
Matches 82; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 395 GTGGCGCTAGCGCAACGGGTCACTACCGCTACTGGGACTGCTCAAGGCTTCGTCT 454
Db 127 GTGCTGCTTCTGGAAGTGGCCACTTACTCGATCTGGGACTGCTCAAGGCTTCGTCT 186
QY 455 CGTGGCCCGGCAAGGCTAAGTCAAGTCAAGTCAAGTCAAGTCAAGGAGCG 508
Db 187 CTGGAGCGCGAAGGCTAAGTCAAGTCAAGTCAAGTCAAGTCAAGGAGCG 240
RESULT 8
LOCUS BI190362 280 bp mRNA linear EST 10-JUL-2001
DEFINITION h4h07fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides CDNA clone h4h07fs 5', mRNA
sequence.
ACCESSION BI190362
VERSION BI190362.1 GI:14664041
KEYWORDS EST.
SOURCE Fusarium sporotrichioides.
ORGANISM Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.
REFERENCE 1 (bases 1 to 280)
AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
,M. and Roe,B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Other ESTs: h4h07fs.f1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762

Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
303 1e-27 gi|1170140|sp|p45699 PUTATIVE ENDOGLUCANASE TYPE
KPRECURSOR (EN
Seq primer: T3
High quality sequence stop: 261.
FEATURES
source Location/Qualifiers
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/strain="Tri 10"
/db_xref="taxon:5514"
/clone="h4h07fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
XhoI; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 60 a 79 c 53 g 88 t
ORIGIN
Query Match 6.0%; Score 62.8; DB 13; Length 280;
Best Local Similarity 71.9%; Pred. No. 0.0045;
Matches 82; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 395 GTGGCGCTAGCGCAACGGGTCACTACCGCTACTGGGACTGCTCAAGGCTTCGTCT 454
Db 133 GTGCTGCTTCTGGAAGTGGCCACTTACTCGATCTGGGACTGCTCAAGGCTTCGTCT 192
QY 455 CGTGGCCCGGCAAGGCTAAGTCAAGTCAAGTCAAGTCAAGTCAAGGAGCG 508
Db 193 CTGGAGCGCGAAGGCTAAGTCAAGTCAAGTCAAGTCAAGTCAAGGAGCG 246
RESULT 9
LOCUS BI189728 289 bp mRNA linear EST 10-JUL-2001
DEFINITION g1c06fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides CDNA clone g1c06fs 5', mRNA
sequence.
ACCESSION BI189728
VERSION BI189728.1 GI:14663407
KEYWORDS EST.
SOURCE Fusarium sporotrichioides.
ORGANISM Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.
REFERENCE 1 (bases 1 to 289)
AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
,M. and Roe,B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
303 1e-27 gi|1170140|sp|p45699 PUTATIVE ENDOGLUCANASE TYPE
KPRECURSOR (EN
Seq primer: T3
High quality sequence stop: 272.
FEATURES
source Location/Qualifiers
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/clone="g1c06fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"

/db_xref="MaizeDB:635311"
 /db_xref="taxon:4577"
 /clone="PC093211"
 /clone_lib="Maize Mapping Project/DuPont Cornsensus Library"
 /notes="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

BASE COUNT 301 a 528 c 405 g 256 t
 ORIGIN

Query Match 5.7%; Score 59.2; DB 11; Length 1490;
 Best Local Similarity 45.0%; Pred. No. 0.044;
 Matches 223; Conservative 0; Mismatches 273; Indels 0; Gaps 0;
 QY 498 CAACAAGACGCGCTCACCGCTCTTAGCGACTCCAAAGCCCAAGTCCGGCTGCAACGGGG 557
 DB 369 CAAGTAGACTCCACGCTCGGCATCTTCAGCGCGAGTCAAGCCCTGCGGCAACAGC 428
 QY 558 CAATCTTACATGTGCAAGACCAACGCCATGGCTGTCAAGCAACCTTGTTCAGG 617
 DB 429 CATCTTCCTGACGGCAAGTATCAAGTGTGTTCGACGCAACCCAGCAACTGCC 488
 QY 618 TTTCCTCCGCTCCATAGCGCGGTGGCGAGAGCGGTGTGTGTCTCTCTCTTCA 677
 DB 489 GTGGGGGAGCTCGGCATGACCTGTATCGAGGGCAGCGGGCTTCTGTGACCTGG 548
 QY 678 GCTACCTTACCTTCCACCAAGGTGTGTGGCAAGAGATGTGTCTTCAAGTCAACAC 737
 DB 549 GGGCGGGGAAGACATCCAGCGGGGGCCCAAGAGAGTGTCTATCACGGCCCGGCA 608
 QY 738 TGGCGGTGACCTTGGAGCTTCCAGCGTCCAGCGTCCAGTCTTCAATCCAGTCCCGGGGG 797
 DB 609 GGGCGACATCCCACTTACCTGTCTGCGGTCAATGCCGACCAAGTACACCCCGAGGCC 668
 QY 798 CQTGGCATCTTCAAGGATGCTGCTGCCAGTGGGGCTCCCAAGCAGCGGTGGGGCTC 857
 DB 669 CATCATAGCAAGCGCTCTGCAACCAACTGCTCGCGCCATTGTCAAGTCTCTGA 728
 QY 858 GGGCTACGGGGATGCTCCAGCAGACTGTGTGCTCTCCAGCGGCTCCAGGC 917
 DB 729 CCAAGTTCGGGATCATCAAGGGCAACATGACACCACTTCTTACCGGGGACCA 788
 QY 918 CGGCTGCAAGTGGCGCTTCACTGTGTTCAAGAACGCGGACACCCGTTCATGACCTCAA 977
 DB 789 GAGGCTGTGGACGCGAGCACCGGACCTGCGCGCGCGCGCGCGCGCTCAACAT 848
 QY 978 GGAGGTACCTGCGCC 993
 DB 849 COTGCCACATCCACC 864

RESULT 15
 B0743825
 LOCUS
 DEFINITION
 B0743825 490 bp mRNA linear EST 17-JUL-2002
 aestivum cDNA clone WHE4108_E11_J22, mRNA sequence.
 B0743825
 B0743825.1 GI:21890612
 EST.
 bread wheat.
 Triticum aestivum
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 ; Triticeae; Triticum.
 1 (bases 1 to 490)
 Anderson, O.D., Akhunov, E., Chao, S., Crossman, C., Deal, K., Dvorak, J.,
 Lazo, G.R., Pham, J., Rausch, C.J., Wilson, C. and Woo, J.
 The structure and function of the expressed portion of the wheat
 genomes - Salt-stressed root cDNA library

JOURNAL COMMENT

Unpublished (2002)
 Contact: Olin Anderson
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 West Area, Western Regional Research Center
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 Tel: 5105595773
 Fax: 5105595818
 Email: oanderson@w.usda.gov
 Sequences have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: SK primer
 Location/Qualifiers

FEATURES

source

1..490
 /organism="Triticum aestivum"
 /cultivar="Chinese Spring"
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 /dev_stage="Full tillering"
 /lab_host="E. coli SOLR"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid
 pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Hydroponic
 plants grown to full tillering stage were treated with 150
 mM NaCl for either 12 hours or 7 days. Root tissues of the
 plants subjected to both types of treatment were collected
 separately at University of California, Davis (E. Akhunov
 and K. Deal in J. Dvorak's lab). Total RNA was prepared
 and equal amount of RNA was then pooled. PolyA RNA was
 purified from the pooled RNA, a cDNA library was made, and
 the cDNA clones were in vivo excised to give pBluescript
 SK(-) phagemids in J. Dvorak's lab (E. Akhunov, J. Dvorak)
 at the University of California, Davis. Colony plating,
 plasmid DNA preparations and DNA sequencing were performed
 in the OD Anderson lab (all other authors)."

BASE COUNT 85 a 196 c 167 g 42 t
 ORIGIN

Query Match 5.6%; Score 58.4; DB 14; Length 490;
 Best Local Similarity 47.3%; Pred. No. 0.044;
 Matches 176; Conservative 0; Mismatches 196; Indels 0; Gaps 0;
 QY 307 CCGCCAGAGACGACGCGTCCCAAGGCTTCGACTCCGCTCAACTCGAGCAGCTCG 366
 DB 66 CAGCCCTTGGCGCCGAGAGCTCGACAGAGCGGCGCGCGCTCGCGGGCGGC 125
 QY 367 TCTTGGGAAAGTACAGCGTGTACGGGTGGCGTACGGGCAACGGGCTACTACCGC 426
 DB 126 GCGACCGGGCTCGCGCTCGCGCTCGCGCGCGGCAACGGGCGGCGGCGCAC 185
 QY 427 TACTGGGACTGTGCAAGGCTTCGTCTGTGGCCCGGCAAGGCTAACGTGAGCTCGCCT 486
 DB 186 TACCGCGCGTCAGAGAGCGCGCTGGGGCGGTATACGGCGGAGATCCGCGACCGCGCC 245
 QY 487 GTCAAGTCTGCAAGAGCAGCGGCTCACCGCTCTTAGCGACTCCAAACGCGCAGTCCGGC 546
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 DB 306 GAGCGCGCGCGGAGTACCGCGGCAACAGGCGACAGCACTTCCCTTCGCTCC 365
 QY 607 CTTGCTTACGGTTTGGTGGCGGTGCGATTAGCGGGGTGGGAGAGCGGCTGGTGTG 666
 DB 366 GCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCTTACCGCGGAGCGCGGCAACAGC 425
 QY 667 TCTGCTTTCGAG 678
 DB 426 AGCACCCTCGAG 437.

Search completed: June 18, 2003, 03:16:31

Wed Jun 18 17:55:22 2003

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Job time : 1503 secs

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